

## SEQUENCE LISTING

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<120> Leucine rich repeat containing protein

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<151> 2004-02-12

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<170> SeqWin99, version 1.02

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<212> DNA

<213> Homo sapiens

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Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe 20 25 30

Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe 35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr 50 55 60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr 65 70 75 80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu 85 90 95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu 100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu 115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
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Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
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Ser Asp Thr Pro Lys Gly  
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Ile Leu Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu  
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Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala  
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Phe Lys Asp Leu Lys Leu Gln  
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 20 25 30

Asn Trp Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser

35 40 45

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20							25				30				

Ser	Lys	Ala	Glu	Arg	Pro	Gln	Gly	Gly	Arg	His	Thr	Gly	Ile	Ser	Thr
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Leu	Gly	Lys	Lys	Ala	Lys	Ala	Gly	Ser	Gly	Leu	Arg	Lys	Lys	Gln	Arg
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Arg Leu Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln Ala Ala Gly  
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Lys Lys Glu Asp Ala Pro Gln Asp Leu Ala Leu Ala Val Cys Leu Ser  
85 90 95

Val Phe Ile Thr Phe Leu Val Ala Phe Ser Leu Gly Ala Phe Thr Arg  
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Pro Tyr Val Asp Arg Leu Trp Gln Lys Lys Cys Gln Ser Lys Ser Pro  
115 120 125

Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly Phe Tyr Asp Asp Met Glu  
130 135 140

Ala Ala Gly His Thr Pro His Pro Glu Thr His Leu Arg Gln Val Phe  
145 150 155 160

Pro His Leu Ser Leu Tyr Glu Asn Gln Thr Pro Phe Trp Val Thr Gln  
165 170 175

Pro His Pro His Ala Thr Val Ile Pro Asp Arg Thr Leu Gly Arg Ser  
180 185 190

Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro Gly Gln Cys Gly Asp Asn  
195 200 205

Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala Val Tyr Ser Ile Leu Gln  
210 215 220

Arg His Pro His Ala Gly Asn Arg Glu Leu Met Ser Ala Ala Gln Asp  
225 230 235 240

His Ile His Arg Asn Asp Ile Leu Gly Glu Trp Thr Tyr Glu Thr Val  
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Ala Gln Glu Glu Pro Leu Ser Ala His Ser Val Gly Val Ser Ser Val  
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Ala Gly Thr Ser His Ala Val Ser Gly Ser Ser Arg Tyr Asp Ser Asn  
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Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile Thr Ala Ser Leu Cys Lys  
290 295 300

Met Leu Thr His Ala Glu Ala Gln Arg Thr Gly Asp Ser Lys Glu Arg  
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Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser Gln Met Glu Phe Ser Lys  
325 330 335

Glu Arg Gln Val Ser Ser Ser Ile Asp Leu Leu Ser Ile Gln Gln Pro  
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Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala Leu Ser Ala His Tyr Ser  
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Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr Gly Pro Ser Val Phe Pro  
370 375 380

Pro Arg Trp Asp Ser Gly Leu Asp Val Thr Pro Ala Asn Lys Glu Pro

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405	410	415	
Cys Asp Ser Asp Glu Gly Ser Leu Phe Thr Leu Ser Ser Ile Ser Ser			
420	425	430	
Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala Val Pro Asp Glu Glu Ser			
435	440	445	
Leu Gln Asp Glu Ser Ser Gly Ala Ser Lys Asp Asn Val Thr Ala Val			
450	455	460	
Asp Ser Leu Glu Glu Asn Val Thr Phe Gln Thr Ile Pro Gly Lys Cys			
465	470	475	480
Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro Leu Ile Ser Ala Pro Asp			
485	490	495	
Ser Gly Met Tyr Lys Thr His Leu Glu Asn Ala Ser Asp Thr Asp Arg			
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Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser Pro Gly Asn Ser Pro Leu			
515	520	525	
Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu			
530	535	540	
Gln Ser Lys Ala Ala Glu Trp His Cys Ser Leu Arg Asp Leu Glu Phe			
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Pro Ser Asp Pro Asp Lys Ala Ala			
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&lt;211&gt; 870

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

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				20				25					30		

Asn	Ser	Glu	Cys	Gln	Trp	Asn	Glu	Tyr	Ile	Leu	Thr	Asn	Cys	Ser	Phe
		35				40						45			

Thr	Gly	Lys	Cys	Asp	Ile	Pro	Val	Asp	Ile	Ser	Gln	Thr	Ala	Ala	Thr
		50			55					60					

Val	Asp	Val	Ser	Phe	Asn	Phe	Phe	Arg	Val	Leu	Leu	Gln	Ser	His	Thr
65				70				75					80		

Lys	Lys	Glu	Glu	Trp	Lys	Ile	Lys	His	Leu	Asp	Leu	Ser	Asn	Asn	Leu
		85					90					95			

Ile	Ser	Lys	Ile	Thr	Leu	Ser	Pro	Phe	Ala	Tyr	Leu	His	Ala	Leu	Glu
		100			105							110			

Val	Leu	Asn	Leu	Ser	Asn	Ala	Ile	His	Ser	Leu	Ser	Leu	Asp	Leu	
	115				120				125						

Leu	Ser	Pro	Lys	Ser	Ser	Trp	Val	Lys	Arg	His	Arg	Ser	Ser	Phe	Arg
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Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
145 150 155 160

Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu  
165 170 175

Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His  
180 185 190

Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe  
195 200 205

Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile  
210 215 220

Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile  
225 230 235 240

Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp  
245 250 255

Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser  
260 265 270

Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu  
275 280 285

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
290 295 300

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
305 310 315 320

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
325 330 335

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
340 345 350

Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln Ala Ala Gly Lys Lys  
355 360 365

Glu Asp Ala Pro Gln Asp Leu Ala Leu Ala Val Cys Leu Ser Val Phe  
370 375 380

Ile Thr Phe Leu Val Ala Phe Ser Leu Gly Ala Phe Thr Arg Pro Tyr  
385 390 395 400

Val Asp Arg Leu Trp Gln Lys Lys Cys Gln Ser Lys Ser Pro Gly Leu  
405 410 415

Asp Asn Ala Tyr Ser Asn Glu Gly Phe Tyr Asp Asp Met Glu Ala Ala  
420 425 430

Gly His Thr Pro His Pro Glu Thr His Leu Arg Gln Val Phe Pro His  
435 440 445

Leu Ser Leu Tyr Glu Asn Gln Thr Pro Phe Trp Val Thr Gln Pro His  
450 455 460

Pro His Ala Thr Val Ile Pro Asp Arg Thr Leu Gly Arg Ser Arg Lys

465 470 475 480

Asp Pro Gly Ser Ser Gln Ser Pro Gly Gln Cys Gly Asp Asn Thr Gly  
485 490 495

Ala Gly Ser Gly Asn Asp Gly Ala Val Tyr Ser Ile Leu Gln Arg His  
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Pro His Ala Gly Asn Arg Glu Leu Met Ser Ala Ala Gln Asp His Ile  
515 520 525

His Arg Asn Asp Ile Leu Gly Glu Trp Thr Tyr Glu Thr Val Ala Gln  
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Glu Glu Pro Leu Ser Ala His Ser Val Gly Val Ser Ser Val Ala Gly  
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Thr Ser His Ala Val Ser Gly Ser Ser Arg Tyr Asp Ser Asn Glu Leu  
565 570 575

Asp Pro Ser Leu Ser Gly Glu Ile Thr Ala Ser Leu Cys Lys Met Leu  
580 585 590

Thr His Ala Glu Ala Gln Arg Thr Gly Asp Ser Lys Glu Arg Gly Gly  
595 600 605

Thr Glu Gln Ser Leu Trp Asp Ser Gln Met Glu Phe Ser Lys Glu Arg  
610 615 620

Gln Val Ser Ser Ser Ile Asp Leu Leu Ser Ile Gln Gln Pro Arg Leu  
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Ser Gly Ala Arg Ala Glu Glu Ala Leu Ser Ala His Tyr Ser Glu Val  
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Pro Tyr Gly Asp Pro Arg Asp Thr Gly Pro Ser Val Phe Pro Pro Arg  
660 665 670

Trp Asp Ser Gly Leu Asp Val Thr Pro Ala Asn Lys Glu Pro Val Gln  
675 680 685

Lys Ser Thr Pro Ser Asp Thr Cys Cys Glu Leu Glu Ser Asp Cys Asp  
690 695 700

Ser Asp Glu Gly Ser Leu Phe Thr Leu Ser Ser Ile Ser Ser Glu Ser  
705 710 715 720

Ala Arg Ser Lys Thr Glu Glu Ala Val Pro Asp Glu Glu Ser Leu Gln  
725 730 735

Asp Glu Ser Ser Gly Ala Ser Lys Asp Asn Val Thr Ala Val Asp Ser  
740 745 750

Leu Glu Glu Asn Val Thr Phe Gln Thr Ile Pro Gly Lys Cys Lys Asn  
755 760 765

Gln Glu Asp Pro Phe Glu Lys Pro Leu Ile Ser Ala Pro Asp Ser Gly  
770 775 780

Met Tyr Lys Thr His Leu Glu Asn Ala Ser Asp Thr Asp Arg Ser Glu  
785 790 795 800

Gly Leu Ser Pro Trp Pro Arg Ser Pro Gly Asn Ser Pro Leu Gly Asp  
 805 810 815

Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu Gln Ser  
 820 825 830

Lys Ala Ala Glu Trp His Cys Ser Leu Arg Asp Leu Glu Phe Ser Asn  
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Val Asp Val Leu Gln Gln Thr Pro Pro Cys Ser Ala Glu Val Pro Ser  
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Asp Pro Asp Lys Ala Ala  
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 <212> DNA  
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 20 25 30

Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly  
 130 135 140

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<212> DNA

<213> Homo sapiens

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<212> PRT

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35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp  
130 135 140

Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu  
145 150 155 160

Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu  
165 170 175

Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys  
180 185 190

Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile  
195 200 205

Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val  
210 215 220

Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val  
225 230 235 240

Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile  
245 250 255

Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
260 265 270

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
275 280 285

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
290 295 300

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
305 310 315 320

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
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370 375 380

Cys Gln Ser Lys Ser Pro Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly  
385 390 395 400

Phe Tyr Asp Asp Met Glu Ala Ala Gly His Thr Pro His Pro Glu Thr  
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His Leu Arg Gln Val Phe Pro His Leu Ser Leu Tyr Glu Asn Gln Thr  
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Pro Phe Trp Val Thr Gln Pro His Pro His Ala Thr Val Ile Pro Asp  
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Arg Thr Leu Gly Arg Ser Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro  
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Gly Gln Cys Gly Asp Asn Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala  
465 470 475 480

Val Tyr Ser Ile Leu Gln Arg His Pro His Ala Gly Asn Arg Glu Leu  
485 490 495

Met Ser Ala Ala Gln Asp His Ile His Arg Asn Asp Ile Leu Gly Glu  
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Trp Thr Tyr Glu Thr Val Ala Gln Glu Glu Pro Leu Ser Ala His Ser  
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Val Gly Val Ser Ser Val Ala Gly Thr Ser His Ala Val Ser Gly Ser  
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Ser Arg Tyr Asp Ser Asn Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile  
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Thr Ala Ser Leu Cys Lys Met Leu Thr His Ala Glu Ala Gln Arg Thr  
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Gly Asp Ser Lys Glu Arg Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser  
580 585 590

Gln Met Glu Phe Ser Lys Glu Arg Gln Val Ser Ser Ser Ile Asp Leu  
595 600 605

Leu Ser Ile Gln Gln Pro Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala  
610 615 620

Leu Ser Ala His Tyr Ser Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr  
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Gly Pro Ser Val Phe Pro Pro Arg Trp Asp Ser Gly Leu Asp Val Thr  
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Pro Ala Asn Lys Glu Pro Val Gln Lys Ser Thr Pro Ser Asp Thr Cys

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675	680	685
Leu Ser Ser Ile Ser Ser Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala		
690	695	700
Val Pro Asp Glu Glu Ser Leu Gln Asp Glu Ser Ser Gly Ala Ser Lys		
705	710	715
Asp Asn Val Thr Ala Val Asp Ser Leu Glu Glu Asn Val Thr Phe Gln		
725	730	735
Thr Ile Pro Gly Lys Cys Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro		
740	745	750
Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn		
755	760	765
Ala Ser Asp Thr Asp Arg Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser		
770	775	780
Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr		
785	790	795
800		
Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser		
805	810	815
Leu Arg Asp Leu Glu Phe Ser Asn Val Asp Val Leu Gln Gln Thr Pro		
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<212> PRT  
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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
35 40 45  
Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr  
50 55 60  
Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr  
65 70 75 80  
Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
85 90 95  
Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu  
100 105 110  
Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
115 120 125  
Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
130 135 140  
Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
145 150 155 160  
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165 170 175  
Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His  
180 185 190  
Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe  
195 200 205  
Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile  
210 215 220  
Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile  
225 230 235 240  
Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp  
245 250 255  
Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser  
260 265 270  
Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu  
275 280 285  
Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg

290	295	300	
Leu Pro Pro Ile His Leu His Arg Met Lys Ser	Leu Ile Arg Ser Lys		
305	310	315	320
Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly	Ile Ser Thr Leu Gly		
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Lys Lys Ala Lys Ala Gly Ser Gly	Leu Arg Lys Lys Gln Arg Arg Leu		
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Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe			
20	25		30
Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe			
35	40		45
Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr			
50	55		60
Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr			
65	70		75
80			
Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu			
85	90		95
Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu			
100	105		110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
 115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
 130 135 140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
 145 150 155 160

Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
 165 170 175

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
 180 185 190

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
 195 200 205

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
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Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
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Asp Val Gln

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<212> DNA

<213> Homo sapiens

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<211> 339

<212> PRT

<213> Homo sapiens

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Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe			
35	40	45	
Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys			
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His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro			
65	70	75	80
Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala			
85	90	95	
Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val			
100	105	110	
Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val			
115	120	125	
Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp			
130	135	140	
Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu			
145	150	155	160
Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu			
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Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys			
180	185	190	
Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile			
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Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val			
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Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val			
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Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile			
245	250	255	
Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln			
260	265	270	
Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg			
275	280	285	
Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg			
290	295	300	
His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly			
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Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg			
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Asp Val Gln			

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Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
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Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu  
 130 135 140

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 145 150 155 160

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 165 170 175

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
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Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
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Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln  
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gcagagaggc cccaggggagg aaggcacacg 900  
gcgggctctg gtctcaggaa gaagcagaga 960  
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gatcttggca gttcgcagag cccaggacag 1380  
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acgtctcagc ctgtctctgg ctcaagccgt 1620  
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cttagagact tagaattttc aaatgtggac 2460  
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<211> 876

<212> PRT

<213> Artificial Sequence

<220>

<223> histidine tagged INSP179 polypeptide sequence

<400> 24

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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr  
50 55 60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr  
65 70 75 80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
85 90 95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu  
100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
130 135 140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
145 150 155 160

Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu  
165 170 175

Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His  
180 185 190

Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe  
195 200 205

Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile  
210 215 220

Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile  
225 230 235 240

Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp  
245 250 255

Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser  
260 265 270

Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu  
275 280 285

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
290 295 300

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
305 310 315 320

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
325 330 335

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
340 345 350

Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln Ala Ala Gly Lys Lys  
355 360 365

Glu Asp Ala Pro Gln Asp Leu Ala Leu Ala Val Cys Leu Ser Val Phe  
370 375 380

Ile Thr Phe Leu Val Ala Phe Ser Leu Gly Ala Phe Thr Arg Pro Tyr  
385 390 395 400

Val Asp Arg Leu Trp Gln Lys Lys Cys Gln Ser Lys Ser Pro Gly Leu  
405 410 415

Asp Asn Ala Tyr Ser Asn Glu Gly Phe Tyr Asp Asp Met Glu Ala Ala  
420 425 430

Gly His Thr Pro His Pro Glu Thr His Leu Arg Gln Val Phe Pro His  
435 440 445

Leu Ser Leu Tyr Glu Asn Gln Thr Pro Phe Trp Val Thr Gln Pro His  
450 455 460

Pro His Ala Thr Val Ile Pro Asp Arg Thr Leu Gly Arg Ser Arg Lys  
465 470 475 480

Asp Pro Gly Ser Ser Gln Ser Pro Gly Gln Cys Gly Asp Asn Thr Gly  
485 490 495

Ala Gly Ser Gly Asn Asp Gly Ala Val Tyr Ser Ile Leu Gln Arg His  
500 505 510

Pro His Ala Gly Asn Arg Glu Leu Met Ser Ala Ala Gln Asp His Ile  
515 520 525

His Arg Asn Asp Ile Leu Gly Glu Trp Thr Tyr Glu Thr Val Ala Gln  
530 535 540

Glu Glu Pro Leu Ser Ala His Ser Val Gly Val Ser Ser Val Ala Gly  
545 550 555 560

Thr Ser His Ala Val Ser Gly Ser Ser Arg Tyr Asp Ser Asn Glu Leu  
565 570 575

Asp Pro Ser Leu Ser Gly Glu Ile Thr Ala Ser Leu Cys Lys Met Leu  
580 585 590

Thr His Ala Glu Ala Gln Arg Thr Gly Asp Ser Lys Glu Arg Gly Gly  
595 600 605

Thr Glu Gln Ser Leu Trp Asp Ser Gln Met Glu Phe Ser Lys Glu Arg  
610 615 620

Gln Val Ser Ser Ser Ile Asp Leu Leu Ser Ile Gln Gln Pro Arg Leu  
625 630 635 640

Ser Gly Ala Arg Ala Glu Glu Ala Leu Ser Ala His Tyr Ser Glu Val  
645 650 655

Pro Tyr Gly Asp Pro Arg Asp Thr Gly Pro Ser Val Phe Pro Pro Arg  
660 665 670

Trp Asp Ser Gly Leu Asp Val Thr Pro Ala Asn Lys Glu Pro Val Gln  
675 680 685

Lys Ser Thr Pro Ser Asp Thr Cys Cys Glu Leu Glu Ser Asp Cys Asp  
690 695 700

Ser Asp Glu Gly Ser Leu Phe Thr Leu Ser Ser Ile Ser Ser Glu Ser  
705 710 715 720

Ala Arg Ser Lys Thr Glu Glu Ala Val Pro Asp Glu Glu Ser Leu Gln  
725 730 735

Asp Glu Ser Ser Gly Ala Ser Lys Asp Asn Val Thr Ala Val Asp Ser  
740 745 750

Leu Glu Glu Asn Val Thr Phe Gln Thr Ile Pro Gly Lys Cys Lys Asn  
755 760 765

Gln Glu Asp Pro Phe Glu Lys Pro Leu Ile Ser Ala Pro Asp Ser Gly  
770 775 780

Met Tyr Lys Thr His Leu Glu Asn Ala Ser Asp Thr Asp Arg Ser Glu  
785 790 795 800

Gly Leu Ser Pro Trp Pro Arg Ser Pro Gly Asn Ser Pro Leu Gly Asp  
805 810 815

Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu Gln Ser  
820 825 830

Lys Ala Ala Glu Trp His Cys Ser Leu Arg Asp Leu Glu Phe Ser Asn  
835 840 845

Val Asp Val Leu Gln Gln Thr Pro Pro Cys Ser Ala Glu Val Pro Ser  
850 855 860

Asp Pro Asp Lys Ala Ala His His His His His His  
865 870 875

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tcattggatc tactcagtcc	taagtccctca	tggtgaaac	gccacagaag	cagcttcaga	360
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ccccatctag tggttgactt	ggctgataat	aactggcagt	gtgatgatag	tgtggcagtc	720
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&lt;210&gt; 26

&lt;211&gt; 852

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; histidine tagged INSP179 mature polypeptide sequence

&lt;400&gt; 26

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35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp  
130 135 140

Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu  
145 150 155 160

Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu  
165 170 175

Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys  
180 185 190

Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile  
195 200 205

Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val  
210 215 220

Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val  
225 230 235 240

Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile  
245 250 255

Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
260 265 270

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
275 280 285

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
290 295 300

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
305 310 315 320

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
325 330 335

Asp Val Gln Ala Ala Gly Lys Lys Glu Asp Ala Pro Gln Asp Leu Ala  
340 345 350

Leu Ala Val Cys Leu Ser Val Phe Ile Thr Phe Leu Val Ala Phe Ser  
355 360 365

Leu Gly Ala Phe Thr Arg Pro Tyr Val Asp Arg Leu Trp Gln Lys Lys

370                   375                   380  
Cys Gln Ser Lys Ser Pro Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly  
385                   390                   395                   400  
Phe Tyr Asp Asp Met Glu Ala Ala Gly His Thr Pro His Pro Glu Thr  
405                   410                   415  
His Leu Arg Gln Val Phe Pro His Leu Ser Leu Tyr Glu Asn Gln Thr  
420                   425                   430  
Pro Phe Trp Val Thr Gln Pro His Pro His Ala Thr Val Ile Pro Asp  
435                   440                   445  
Arg Thr Leu Gly Arg Ser Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro  
450                   455                   460  
Gly Gln Cys Gly Asp Asn Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala  
465                   470                   475                   480  
Val Tyr Ser Ile Leu Gln Arg His Pro His Ala Gly Asn Arg Glu Leu  
485                   490                   495  
Met Ser Ala Ala Gln Asp His Ile His Arg Asn Asp Ile Leu Gly Glu  
500                   505                   510  
Trp Thr Tyr Glu Thr Val Ala Gln Glu Glu Pro Leu Ser Ala His Ser  
515                   520                   525  
Val Gly Val Ser Ser Val Ala Gly Thr Ser His Ala Val Ser Gly Ser  
530                   535                   540  
Ser Arg Tyr Asp Ser Asn Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile  
545                   550                   555                   560  
Thr Ala Ser Leu Cys Lys Met Leu Thr His Ala Glu Ala Gln Arg Thr  
565                   570                   575  
Gly Asp Ser Lys Glu Arg Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser  
580                   585                   590  
Gln Met Glu Phe Ser Lys Glu Arg Gln Val Ser Ser Ser Ile Asp Leu  
595                   600                   605  
Leu Ser Ile Gln Gln Pro Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala  
610                   615                   620  
Leu Ser Ala His Tyr Ser Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr  
625                   630                   635                   640  
Gly Pro Ser Val Phe Pro Pro Arg Trp Asp Ser Gly Leu Asp Val Thr  
645                   650                   655  
Pro Ala Asn Lys Glu Pro Val Gln Lys Ser Thr Pro Ser Asp Thr Cys  
660                   665                   670  
Cys Glu Leu Glu Ser Asp Cys Asp Ser Asp Glu Gly Ser Leu Phe Thr  
675                   680                   685  
Leu Ser Ser Ile Ser Ser Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala  
690                   695                   700

Val	Pro	Asp	Glu	Glu	Ser	Leu	Gln	Asp	Glu	Ser	Ser	Gly	Ala	Ser	Lys
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Asp Asn Val Thr Ala Val Asp Ser Leu Glu Glu Asn Val Thr Phe Gln															
															725 730 735
Thr Ile Pro Gly Lys Cys Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro															
															740 745 750
Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn															
															755 760 765
Ala Ser Asp Thr Asp Arg Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser															
															770 775 780
Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr															
															785 790 795 800
Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser															
															805 810 815
Leu Arg Asp Leu Glu Phe Ser Asn Val Asp Val Leu Gln Gln Thr Pro															
															820 825 830
Pro Cys Ser Ala Glu Val Pro Ser Asp Pro Asp Lys Ala Ala His His															
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His His His His															
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<212> PRT

<213> Artificial Sequence

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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr  
50 55 60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr  
65 70 75 80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
85 90 95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu  
100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
130 135 140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
145 150 155 160

Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu  
165 170 175

Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His  
180 185 190

Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe  
195 200 205

Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile  
210 215 220

Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile  
225 230 235 240

Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp  
245 250 255

Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser  
260 265 270

Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu  
275 280 285

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 290 295 300

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 305 310 315 320

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
 325 330 335

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
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<211> 747

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<213> Artificial Sequence

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 gcagagaggc cccaggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaaag 660  
 gcccggctctg gtctcaggaa gaagcagaga cggctgccaa ggagtgttag aagcacccgc 720  
 gatgtgcagc accatcacca tcaccat 747

<210> 30

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> histidine tagged INSP179-EC-SV1 polypeptide sequence

<400> 30

Met Lys Asn Leu Tyr Phe Arg Val Ile Thr Ile Val Ile Gly Leu Tyr  
 1 5 10 15

Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe  
 20 25 30

Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
 35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr

50	55	60	
Val Asp Val Ser Phe Asn Phe Phe Arg Val	Leu Leu Gln Ser His Thr		
65	70	75	80
Lys Lys Glu Glu Trp Lys Ile Lys His	Leu Asp Leu Ser Asn Asn Leu		
85	90	95	
Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala	Tyr Leu His Ala Leu Glu		
100	105	110	
Val Leu Asn Leu Ser Asn Asn Ala Ile His	Ser Leu Ser Leu Asp Leu		
115	120	125	
Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His	Arg Ser Ser Phe Arg		
130	135	140	
Asn Arg Phe Pro Leu Leu Lys Val Leu Ile	Leu Gln Arg Asn Lys Leu		
145	150	155	160
Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn	Gly Gly Thr Pro Gln		
165	170	175	
Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro	Pro Ile His Leu His Arg		
180	185	190	
Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg	Pro Gln Gly Gly Arg		
195	200	205	
His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala	Lys Ala Gly Ser Gly		
210	215	220	
Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg	Ser Val Arg Ser Thr Arg		
225	230	235	240
Asp Val Gln His His His His His His			
245			
<210> 31			
<211> 1035			
<212> DNA			
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<220>			
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<400> 31			
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gtggatgtaa gtttcaatt cttagatgtt ctcttacagt ctcacacgaa aaaagaagag			
tggaaaataaa aacatctgaa cctcagtaac aatctcatat caaaaataac cttaaaggcc			
tttgcataatt tacatgtttt ggaagtgtta aacctcagca acaatgccat ccactccctc			
tcattggatc tactcagttc taagtctca tgggtgaaac gcccacagaag cagttcaga			
aacaggtttc cattgtctgaa ggtgctcatt cttcaaaagaa ataaaactcag tgacactccc			
aaggggactgt ggaaactgaa gtcattgcag agtttggatc tgcattcaa tggatattg			
caaataagggt ggtctgatt tcacaactgc ctgcaactgg agaatctctg tttaaagagc			
aacaagatat taaaattcc cccacaagcc ttcaaggacc tcaaaaaatt acaggtcata			
gaccttagca acaatgtct gattaccatc ctaccaatga tgatcatgc tctagaattt			
ccccatctag tgggtgactt ggctgataat aactggcagt gtgatgatag tgcggcagtc			
tttcaaaatt ttatctgaa atcctggagg aaaaagtgaa atgtcatttg caacaggtct			
ataggggatg aggaggccaa cggggcact cccagagca ggatttccag ggaaacccgc			
840			

cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 900  
 cagggaggaa ggcacacggg catttctact ctggggaga aggcaaaggc cggctctgg 960  
 ctcaggaaga agcagagacg gctgccaagg agtgttagaa gcacccgcga tgtgcagcac 1020  
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<210> 32  
 <211> 345  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 32  
 Ser Arg Lys Ser Asn Ile Leu Phe Asn Ser Glu Cys Gln Trp Asn Glu  
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Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val  
 20 25 30

Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp  
 130 135 140

Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu  
 145 150 155 160

Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu  
 165 170 175

Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys  
 180 185 190

Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile  
 195 200 205

Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val  
 210 215 220

Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val  
 225 230 235 240

Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile  
 245 250 255

Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
 260 265 270

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
 275 280 285

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
 290 295 300

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
 305 310 315 320

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
 325 330 335

Asp Val Gln His His His His His  
 340 345

<210> 33  
 <211> 675  
 <212> DNA  
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<220>  
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<400> 33  
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 gtggatgtaa gtttcaattt cttagagtt ctcttacagt ctcacacgaa aaaagaagag 180  
 tggaaaaataa aacatctgga ccttagtaac aatctcataat caaaaataaac cttaaaggccct 240  
 tttgcattt tacatgcttt ggaagtgtta aacctcagca acaaattgccc ccactccctc 300  
 tcattggatc tactcagtcc taagtctca tgggtgaaac gcccacagaag cagcttcaga 360  
 aacagtttc cattgctgaa ggtgctcatt cttcaaagaa ataaaactcaag tgacactccc 420  
 aaggggagtg aggaggccaa cgggggcaact ccccaagagca ggatttccag ggaaacccgc 480  
 cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 540  
 cagggaggaa ggcacacggg catttctact ctggggaaaga aggcaaaaggc cggctctggt 600  
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 catcaccatc accat 675

<210> 34  
 <211> 225  
 <212> PRT  
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<220>  
 <223> histidine tagged INSP179-EC-SV1 mature polypeptide sequence

<400> 34  
 Ser Arg Lys Ser Asn Ile Leu Phe Asn Ser Glu Cys Gln Trp Asn Glu  
 1 5 10 15

Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val  
 20 25 30

Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80

Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125

Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu  
 130 135 140

Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 145 150 155 160

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 165 170 175

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
 180 185 190

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
 195 200 205

Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln His His His His His  
 210 215 220

His  
 225

,

<210> 35  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> linker sequence

<400> 35  
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 1 5 10

<210> 36  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer INSP179-CP1

<400> 36  
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<210> 37  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Primer INSP179-CP2

<400> 37  
ctgcacatcg cgggtgcttc taac 24

<210> 38  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179EC-EX1

<400> 38  
gcaggcttcg ccaccatgaa aaacctctat tttag 35

<210> 39  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179EC-EX2

<400> 39  
tgatggtgat ggtgctgcac atcgcggtg cttct 35

<210> 40  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179-SP1

<400> 40  
atgaaaaacc tctatttcag agtcattac 29

<210> 41  
<211> 20  
<212> DNA  
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<220>  
<223> Primer INSP179-SP2

<400> 41  
caagcattca aggacctcaa 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179-SP3

<400> 42  
catgcgatgc agatgaatgg 20

<210> 43  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer GCP Forward

<400> 43  
ggggacaagt ttgtacaaaa aaggaggctt cgccacc 37

<210> 44  
<211> 51  
<212> DNA  
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<220>  
<223> Primer GCP Reverse

<400> 44  
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<210> 45  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer pEAK12F

<400> 45  
gccagcttgg cacttgatgt 20

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer pEAK12R

<400> 46  
gatggaggtg gacgtgtcag 20

<210> 47  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer 21M13

<400> 47  
tgtaaaacga cggccagt 18

<210> 48  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer M13REV

<400> 48  
cagggaaacag ctatgacc 18

<210> 49  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer T7

<400> 49  
taatacgact cactatagg 19

<210> 50  
<211> 18  
<212> DNA  
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<220>  
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<400> 50  
attnaacccctc actaaagg 18